



SEQUENCE LISTING

<110> KAKIMOTO, TATSUO
HIGUCHI, MASAYUKI
INOUE, TSUTOMU

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
TO CYTOKININ RECEPTOR

<130> Q65478

<140> 09/918,508

<141> 2001-08-01

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<151> 2001-03-15

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<170> PatentIn Ver. 2.1

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His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys	
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Trp	Trp	Cys	Leu	Ile	Leu	Gly	Val	Leu	Val	Cys	His	Lys	Ile	Tyr	Val	
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Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly	
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Tyr	Ala	Pro	Val	Ile	Phe	Ala	Gln	Asp	Thr	Val	Ser	His	Val	Val	Ser	
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Thr	Asn	Arg	Leu	Gly	Val	Ile	Leu	Thr	Phe	Ala	Val	Tyr	Lys	Arg	Asp	
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Tyr	Leu	Gly	Gly	Val	Phe	Asp	Ile	Glu	Ser	Leu	Val	Glu	Asn	Leu	Leu	
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caa	cag	ctg	gct	agc	aag	caa	acg	att	ctt	gtc	aat	gtg	tac	gat	atc	1056
Gln	Gln	Leu	Ala	Ser	Lys	Gln	Thr	Ile	Leu	Val	Asn	Val	Tyr	Asp	Ile	
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Ala	His	Ile	Ile	His	Ala	Thr	Val	Ser	Arg	Ile	His	Lys	Val	Glu	Glu	
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Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser	
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Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly	
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Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly	
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Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met	
245 250 255	
atg tca ggc gag gag gat cgt gag aat att ttg cga gct aga gaa acc	816
Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr	
260 265 270	
gga aaa gct gtc ttg act agc cct ttt agg ttg ttg gaa act cac cat	864
Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His	
275 280 285	
ctc gga gtt gtg ttg aca ttc cct gtc tac aag tct tct ctt cct gaa	912
Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu	
290 295 300	
aat ccg act gtc gaa gag cgt att gca gcc act gca ggg tac ctt ggt	960
Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly	
305 310 315 320	
ggg ggc ttt gat gtg gag tct cta gtc gag aat tta ctt ggt cag ctt	1008
Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu	
325 330 335	
gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca	1056
Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala	
340 345 350	
tca gat cca ctt gtc atg tat ggt aat caa gat gaa gaa gcc gac aga	1104
Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg	
355 360 365	

tct	ctc	tct	cat	gag	agc	aag	ctc	gat	ttt	gga	gac	ccc	ttc	agg	aaa	1152
Ser	Leu	Ser	His	Glu	Ser	Lys	Leu	Asp	Phe	Gly	Asp	Pro	Phe	Arg	Lys	
	370					375					380					
cat	aag	atg	ata	tgc	agg	tac	cac	caa	aag	gca	cca	ata	cca	ttg	aat	1200
His	Lys	Met	Ile	Cys	Arg	Tyr	His	Gln	Lys	Ala	Pro	Ile	Pro	Leu	Asn	
	385				390					395					400	
gtg	ctc	aca	act	gtg	cca	ttg	ttc	ttt	gcg	att	ggg	ttc	ttg	gtg	ggg	1248
Val	Leu	Thr	Thr	Val	Pro	Leu	Phe	Phe	Ala	Ile	Gly	Phe	Leu	Val	Gly	
				405					410					415		
tat	ata	ctg	tat	ggg	gca	gct	atg	cac	ata	gta	aaa	gtc	gaa	gat	gat	1296
Tyr	Ile	Leu	Tyr	Gly	Ala	Ala	Met	His	Ile	Val	Lys	Val	Glu	Asp	Asp	
			420					425					430			
ttc	cat	gaa	atg	caa	gag	ctt	aaa	gtg	cga	gca	gaa	gct	gct	gat	gtc	1344
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val	
		435					440					445				
gct	aaa	tcg	cag	ttt	ctt	gct	acc	gtg	tct	cac	gag	atc	agg	aca	cca	1392
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	
	450					455					460					
atg	aat	ggc	att	ctc	gga	atg	ctt	gct	atg	ctc	cta	gat	aca	gaa	cta	1440
Met	Asn	Gly	Ile	Leu	Gly	Met	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu	
	465				470				475						480	
agc	tcg	aca	cag	aga	gat	tac	gct	caa	acc	gct	caa	gta	tgt	ggg	aaa	1488
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys	
				485				490						495		
gct	ttg	att	gca	ttg	ata	aat	gag	gtt	ctt	gat	cgc	gcc	aag	att	gaa	1536
Ala	Leu	Ile	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu	
			500					505					510			
gct	gga	aag	ctg	gag	ttg	gaa	tca	gta	cca	ttt	gat	atc	cgt	tca	ata	1584
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile	
		515					520					525				
ttg	gat	gat	gtc	ctt	tct	cta	ttc	tct	gag	gag	tca	agg	aac	aaa	ggc	1632
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly	
	530					535					540					
att	gag	ctc	gcg	gtt	ttc	gtt	tca	gac	aaa	gta	cca	gag	ata	gtc	aaa	1680
Ile	Glu	Leu	Ala	Val	Phe	Val	Ser	Asp	Lys	Val	Pro	Glu	Ile	Val	Lys	
	545				550				555						560	
gga	gat	tca	ggg	aga	ttt	aga	cag	ata	atc	ata	aac	ctt	gtt	gga	aat	1728
Gly	Asp	Ser	Gly	Arg	Phe	Arg	Gln	Ile	Ile	Ile	Asn	Leu	Val	Gly	Asn	
				565				570						575		
tcg	gtt	aaa	ttc	aca	gag	aaa	gga	cat	atc	ttt	gtt	aaa	gtc	cat	ctt	1776
Ser	Val	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Lys	Val	His	Leu	
			580					585					590			

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly 595 600 605	1824
gga gtg tct gaa gaa atg atc gtt gtt tcc aaa cag tca agt tac aac Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn 610 615 620	1872
aca ttg agc ggt tac gaa gct gct gat ggt cgg aat agc tgg gat tca Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser 625 630 635 640	1920
ttc aag cat ttg gtc tct gag gag cag tca tta tcg gag ttt gat att Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile 645 650 655	1968
tct agc aat gtt agg ctt atg gtt tca atc gaa gac acg ggt att gga Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly 660 665 670	2016
atc cct tta gtt gca caa ggc cgt gtg ttt atg ccg ttt atg caa gca Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala 675 680 685	2064
gat agc tcg act tca aga aac tat gga ggt act ggt att ggt ttg agt Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser 690 695 700	2112
ata agc aag tgt ctt gtt gaa ctt atg cgt ggt cag ata aat ttc ata Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile 705 710 715 720	2160
agc cgg cct cat att gga agc acg ttc tgg ttc acg gct gtt tta gag Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu 725 730 735	2208
aaa tgc gat aaa tgc agt gcg att aac cat atg aag aaa cct aat gtg Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val 740 745 750	2256
gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp 755 760 765	2304
gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu 770 775 780	2352
gga atc aat gtt gat gtc gtg aca agt ctc aaa acc gct gtt gtt gca Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala 785 790 795 800	2400
gct gct gcg ttt gaa aga aac ggt tct cct ctc cca aca aaa ccg caa Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln 805 810 815	2448

ctt gat atg atc tta gta gag aaa gat tca tgg att tca act gaa gat	2496
Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp	
820 825 830	
aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt	2544
Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val	
835 840 845	
cat cac aag tct ccg aaa cta gct cta ttc gca aca aac atc aca aat	2592
His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn	
850 855 860	
tcg gag ttc gac aga gct aaa tcc gca gga ttt gca gat acg gta ata	2640
Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile	
865 870 875 880	
atg aaa ccg tta aga gca agc atg att ggg gcg tgt ctg caa caa gtt	2688
Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val	
885 890 895	
ctc gag ctg aga aaa aca aga caa caa cat cca gaa gga tca tca ccc	2736
Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro	
900 905 910	
gca act ctc aag agc ttg ctt aca ggg aag aag att ctt gtg gtt gat	2784
Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp	
915 920 925	
gat aat ata gtt aac agg aga gta gct gca gga gct ctc aag aaa ttt	2832
Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe	
930 935 940	
gga gca gaa gtg gtt tgt gca gag agt ggt caa gtt gct ttg ggt ttg	2880
Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu	
945 950 955 960	
ctt cag att cca cac act ttc gat gct tgc ttc atg gat att caa atg	2928
Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met	
965 970 975	
cca cag atg gac gga ttt gaa gca act cgt cag ata aga atg atg gag	2976
Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu	
980 985 990	
aag gaa gct aaa gag aag acg aat ctc gaa tgg cat tta ccg att cta	3024
Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu	
995 1000 1005	
gcg atg act gcg gat gtg ata cac gcg acc tac gag gaa tgt ctg aaa	3072
Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys	
1010 1015 1020	
agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc	3120
Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu	
1025 1030 1035 1040	

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168
 Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser
 1045 1050 1055

tcg taa 3174
 Ser

<210> 6
 <211> 1057
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
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 1 5 10 15
 Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser
 20 25 30
 Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys
 35 40 45
 Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys
 50 55 60
 Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn
 65 70 75 80
 Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe
 85 90 95
 Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile
 100 105 110
 Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp
 115 120 125
 Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln
 130 135 140
 Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val
 145 150 155 160
 His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro
 165 170 175
 Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala
 180 185 190
 Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val
 195 200 205
 Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys
 210 215 220
 Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro
 225 230 235 240

Val	Ile	Phe	Ser	Gln	Asp	Ser	Val	Ser	Tyr	Leu	Glu	Ser	Leu	Asp	Met	245	250	255
Met	Ser	Gly	Glu	Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Glu	Thr	260	265	270
Gly	Lys	Ala	Val	Leu	Thr	Ser	Pro	Phe	Arg	Leu	Leu	Glu	Thr	His	His	275	280	285
Leu	Gly	Val	Val	Leu	Thr	Phe	Pro	Val	Tyr	Lys	Ser	Ser	Leu	Pro	Glu	290	295	300
Asn	Pro	Thr	Val	Glu	Glu	Arg	Ile	Ala	Ala	Thr	Ala	Gly	Tyr	Leu	Gly	305	310	315
Gly	Ala	Phe	Asp	Val	Glu	Ser	Leu	Val	Glu	Asn	Leu	Leu	Gly	Gln	Leu	325	330	335
Ala	Gly	Asn	Gln	Ala	Ile	Val	Val	His	Val	Tyr	Asp	Ile	Thr	Asn	Ala	340	345	350
Ser	Asp	Pro	Leu	Val	Met	Tyr	Gly	Asn	Gln	Asp	Glu	Glu	Ala	Asp	Arg	355	360	365
Ser	Leu	Ser	His	Glu	Ser	Lys	Leu	Asp	Phe	Gly	Asp	Pro	Phe	Arg	Lys	370	375	380
His	Lys	Met	Ile	Cys	Arg	Tyr	His	Gln	Lys	Ala	Pro	Ile	Pro	Leu	Asn	385	390	395
Val	Leu	Thr	Thr	Val	Pro	Leu	Phe	Phe	Ala	Ile	Gly	Phe	Leu	Val	Gly	405	410	415
Tyr	Ile	Leu	Tyr	Gly	Ala	Ala	Met	His	Ile	Val	Lys	Val	Glu	Asp	Asp	420	425	430
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val	435	440	445
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	450	455	460
Met	Asn	Gly	Ile	Leu	Gly	Met	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu	465	470	475
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys	485	490	495
Ala	Leu	Ile	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu	500	505	510
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile	515	520	525
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly	530	535	540

Ile	Glu	Leu	Ala	Val	Phe	Val	Ser	Asp	Lys	Val	Pro	Glu	Ile	Val	Lys	545	550	555	560
Gly	Asp	Ser	Gly	Arg	Phe	Arg	Gln	Ile	Ile	Ile	Asn	Leu	Val	Gly	Asn	565	570	575	
Ser	Val	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Lys	Val	His	Leu	580	585	590	
Ala	Glu	Gln	Ser	Lys	Asp	Glu	Ser	Glu	Pro	Lys	Asn	Ala	Leu	Asn	Gly	595	600	605	
Gly	Val	Ser	Glu	Glu	Met	Ile	Val	Val	Ser	Lys	Gln	Ser	Ser	Tyr	Asn	610	615	620	
Thr	Leu	Ser	Gly	Tyr	Glu	Ala	Ala	Asp	Gly	Arg	Asn	Ser	Trp	Asp	Ser	625	630	635	640
Phe	Lys	His	Leu	Val	Ser	Glu	Glu	Gln	Ser	Leu	Ser	Glu	Phe	Asp	Ile	645	650	655	
Ser	Ser	Asn	Val	Arg	Leu	Met	Val	Ser	Ile	Glu	Asp	Thr	Gly	Ile	Gly	660	665	670	
Ile	Pro	Leu	Val	Ala	Gln	Gly	Arg	Val	Phe	Met	Pro	Phe	Met	Gln	Ala	675	680	685	
Asp	Ser	Ser	Thr	Ser	Arg	Asn	Tyr	Gly	Gly	Thr	Gly	Ile	Gly	Leu	Ser	690	695	700	
Ile	Ser	Lys	Cys	Leu	Val	Glu	Leu	Met	Arg	Gly	Gln	Ile	Asn	Phe	Ile	705	710	715	720
Ser	Arg	Pro	His	Ile	Gly	Ser	Thr	Phe	Trp	Phe	Thr	Ala	Val	Leu	Glu	725	730	735	
Lys	Cys	Asp	Lys	Cys	Ser	Ala	Ile	Asn	His	Met	Lys	Lys	Pro	Asn	Val	740	745	750	
Glu	His	Leu	Pro	Ser	Thr	Phe	Lys	Gly	Met	Lys	Ala	Ile	Val	Val	Asp	755	760	765	
Ala	Lys	Pro	Val	Arg	Ala	Ala	Val	Thr	Arg	Tyr	His	Met	Lys	Arg	Leu	770	775	780	
Gly	Ile	Asn	Val	Asp	Val	Val	Thr	Ser	Leu	Lys	Thr	Ala	Val	Val	Ala	785	790	795	800
Ala	Ala	Ala	Phe	Glu	Arg	Asn	Gly	Ser	Pro	Leu	Pro	Thr	Lys	Pro	Gln	805	810	815	
Leu	Asp	Met	Ile	Leu	Val	Glu	Lys	Asp	Ser	Trp	Ile	Ser	Thr	Glu	Asp	820	825	830	
Asn	Asp	Ser	Glu	Ile	Arg	Leu	Leu	Asn	Ser	Arg	Thr	Asn	Gly	Asn	Val	835	840	845	

His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn
 850 855 860
 Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile
 865 870 875 880
 Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val
 885 890 895
 Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro
 900 905 910
 Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp
 915 920 925
 Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe
 930 935 940
 Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu
 945 950 955 960
 Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met
 965 970 975
 Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu
 980 985 990
 Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu
 995 1000 1005
 Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys
 1010 1015 1020
 Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu
 1025 1030 1035 1040
 Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser
 1045 1050 1055

Ser

<210> 7
 <211> 125
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 7
 Glu Thr Ser Val Lys Ile Leu Val Val Glu Asp Asn His Val Asn Gln
 1 5 10 15
 Glu Val Ile Lys Arg Met Leu Asn Leu Glu Gly Ile Glu Asn Ile Glu
 20 25 30
 Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr
 35 40 45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro
 50 55 60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly
 65 70 75 80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn
 85 90 95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro
 100 105 110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe
 115 120 125

<210> 8

<211> 118

<212> PRT

<213> Escherichia coli

<400> 8

Asn Asp Asp Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg
 1 5 10 15

Arg Leu Leu Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr
 20 25 30

Ala Asn Asp Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile
 35 40 45

Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg
 50 55 60

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly
 65 70 75 80

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser
 85 90 95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys
 100 105 110

Gln Ser Leu Thr Leu Tyr
 115

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide primer for PCR

<400> 9

tccccgcgga aaatgttctt acggttaggt ag

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide primer for PCR

<400> 10
 tcggtcgact tatgattctg tatctgaagg cga 33

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide primer for PCR

<400> 11
 tcagatatga actgggcact caac 24

<210> 12
 <211> 24
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide primer for PCR

<400> 12
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<210> 13
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide primer for PCR

<400> 13
 accatgaact gggcactcaa caatcatcaa g 31

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 14

ggattacgac gaaggtgaga taggattagg

30

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 15

gatcccagct agctagggcc ctaccgcggg ga

32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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tccccgcgga aaatgttctt acggttaggt ag

32

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 17

tcggtcgact tatgattctg tatctgaagg cga

33

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 18
ctagtccccg cggtagggcc ctagctagct gg 32

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide primer for PCR

<400> 19
tccccgcgga aaatgtctat aacttgtgag c 31

<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 20
ctagctagct taacaagggtt caaagaatct tgc 33

<210> 21
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 21
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<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide primer for PCR

<400> 22
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